



# The making of The Genoma Music

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## Summary

Both genetic and musical sequences are ordered structures composed of combinations of a small number of elements, of nucleotides and musical notes. In the case of the genome, the emergence of cellular functions makes the order meaningful; in the case of musical sequences, the consequence of order is the production of mysterious esthetical effects in the human mind. Can any musical significance be found in DNA sequence? In this work, we present the technique used to convert DNA sequences into musical sequences. The musical equivalent of the sequence of a number of genes, either of fungal origin, such as *Candida albicans* or *Sacharomyces cerevisiae* (*SLT2*), or belonging to the human genome (genes involved in Alzheimer syndrome, blindness, and deafness such as Connexine 26 gene) has been obtained. Non-coding sequences are also important in life and music. The non-coding aliphoid sequence has also been translated into a musical sequence, in this case using Fibonacci's golden number basic series as structural helper. The elementary musical sequence derived from DNA sequence has served as an imposing frame in which rhythms, sounds, and melodies have been harmonically inserted. The "Genoma Music" Project is essentially a creative metaphor of the basic unity between the human mind and the natural ordered structure of life.

## Key words

Music on the genome, Genome sounds, Musical translation of the DNA code

## Cómo se hizo la Música del Genoma

## Resumen

Tanto las secuencias genéticas como la musicales son estructuras ordenadas compuestas por combinaciones de un pequeño número de elementos, nucleótidos y notas musicales. En el caso del genoma, su consecución final en funciones celulares hace que el orden tenga sentido; en el caso de las secuencias musicales, la consecuencia del orden es la producción de efectos estéticos misteriosos en la mente humana. ¿Puede encontrarse un sentido musical en la secuencia de ADN? En este trabajo presentamos la técnica utilizada para convertir secuencias de ADN en secuencias musicales. Se ha obtenido el equivalente musical de la secuencia de un número de genes, de origen fúngico como *Candida albicans* o *Saccharomyces cerevisiae* (*SLT2*), o que pertenecen al genoma humano (genes relacionados con el síndrome de Alzheimer, ceguera y sordera, como el gen de la conexina 26). También las secuencias no codificantes son importantes en la vida y la música. La secuencia alfoide no codificante ha sido traducida a una secuencia musical, utilizando en este caso la razón aurea de la Sucesión de Fibonacci como ayuda estructural. La secuencia musical elemental derivada de la secuencia de ADN ha servido como un marco donde se han insertado armónicamente ritmos, sonidos y melodías. El Proyecto Musical del Genoma es, esencialmente, una metáfora creativa de la unidad básica entre la mente humana y la estructura ordenada natural de la vida.

## Palabras clave

Música del genoma, Sonidos del genoma, Traducción musical del código de ADN

Using a scale of just four notes that correspond to the four letters of the four nucleotides (ATCG) that form genomic sequences, produces a pleasant, monotonous, and yet surprising sound sequence known as "Genoma Music". Johann Sebastian Bach was the first person to use musical notes linked to four non-musical letters, using the letters of his own last name (B-A-C-H). As with a stream ("bach" means stream), the four notes are sometimes by themselves, sometimes intertwine, repeat, multiply and change harmonies. It is a melodic structure not very far from the "Art of Fuga", which later became the source of inspiration for other composers such as Haendel, Mozart or Beethoven. The latter would eventually give all the musical value to variations that nobody had achieved since Bach.

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Both genetic and musical sequences are ordered structures composed of combinations of a small number of elements, of nucleotides and musical notes. In the case of the genome the emergence of cellular functions makes the order meaningful; in the case of musical sequences, the consequence of the order is the production of mysterious esthetical effects in the human mind. Can any musical significance be found in DNA sequence? In this work, we present the technique used to convert DNA sequences into musical sequences.

The idea originates in 1999, when observing the variations of four elements taken in groups of three from a *Candida albicans* gene; the question thereafter was what would happen if instead of genetic notes these were musical notes? We immediately designed an initial musical experiment using a series of nucleotide triplets corresponding to the series of amino acids, including also the initiation and end codons, representing a sort of complex but fictitious genes (Basic Components Alpha, and Basic Components Omega). This provided a first impression about the musicality of the complex, so that we were ready to select a number of natural genes belonging to *C. albicans*, *Sachromyces cerevisiae* (*SLT2*) and the human species, in these case genes described to be related to severe disabilities.

In March 2001, the first five tracks of this album were released at the Pasteur Institute in Paris, in the memorial celebration for Prof. Edouard Drouhet. The end result has been the creation of 10 tracks, encompassing different styles, which convey emotions and feelings. This project "Genoma Music-1", has been mentioned in over 150 references in the general and specialized domestic and international press [1-50], including the December 2002 issue of the prestigious Science magazine, as a breakthrough initiative ([www.genomamusic.com](http://www.genomamusic.com)).

A musical sequence and a genetic sequence are basic organized elements that acquire a meaning upon their interpretation. If music is one of the most important means of communication, and the expression of each gene yields a protein playing a certain role in the process of life, we are probably trying to communicate in a musical manner "something" in anything and everything that represents life.

## Material and Methods

Starting from such point, we feel that each gene or genetic sequence can be considered as a "musical work" made by Nature. We must bear in mind that this work consists in transforming musical notes, the notes of the genetic score of the different genes. Our material is comprised of two fictitious genes, initially created as a previous step to the work which we shall call "Basic Components Alpha" (BCA), and "Basic Components Omega" (BCO) (tracks 1 through 10 of the CD); two genes of *S. cerevisiae*, *YAL069W* and *SLT2*, the latter having been discovered by the team led by Prof. César Nombela; two non-codifying sequences for proteins, *ALU-J* and *Homo Sapiens* Alphoid sequence; a gene of *C. albicans*, *YRB1P*; three genes related to diseases, such as deafness *Homo sapiens* Connexin 26, blindness *H. sapiens* FASH3 (ELOV4), and Alzheimer's *H. sapiens* protease NEXIN-II.

1) *Analysis of the gene sequence.* A detailed study was done to ascertain the presence and frequency of nucleotide repeats, and the possibility of finding any order in repetitive sequences.

2) *Conversion of genetic notes into musical notes.* In a first intuitive translation of each one of the four genomic letters, A (adenine) became La, C (cytosine) became Do, G (guanine) became Sol, and T (thymine) became Re.

3) *Selection of instruments.* We were able to select the voice of a single instrument, as in the case of the gene Connexin 26, where we used the sound of a bell, or different instruments or sounds corresponding to each one of the four genomic letters. For instance, in the case of the gene *SLT2*, we used a celtic drum, breathing, wood-box, and other effects.

4) *The musical structure of the composition.* Inside each selected tone, the dominant note was determined according to the frequency of each genetic nucleotide in the sequence (see for instance *YRB1* from *C. albicans*). In all coding sequences, the tertiary structure of the nucleotides (determining amino acids or regulatory signals for transcription) forced the use of ternary bar structures. In the case of non-coding sequences, as in the Alphoid sequence, we had a higher degree of freedom to establish the type of bar.

5) *Development of the super-imposed melody.* On the sound sequence obtained from the translation of the genome to musical keys, we have placed rhythms, sounds and a free style melody corresponding to the basic music of the genome. It would be appropriate to use the title "Music on the genome", since the musical theme is built on the gene; it is, in other words, a manner of musically dressing the gene.

Ten tracks were composed using the methodology above:

- *Track 1.* Each chemical base of the genome is converted to a different percussion sound (for instance acute wood block, sidestick, cuica and ride). Tone changes between Re, Mi and Mib. Bar 3/4.
- *Track 2.* Each base corresponds to a note in a voice sound. Tone Dom and bar 3/4.
- *Track 3.* The bass line corresponds to the sequence of bases. This sequence does not encode a protein, enabling higher freedom for the musical expression; a 4/4 bar is applied here.
- *Track 4.* The notes of the sequence correspond to percussion sounds. As in the previous theme, the Alphoid sequence is a non-encoding one. We have provided sense to this sequence applying different note lengths (blowing sounds) accordingly to the Fibonacci's series (golden number) in progressively changing tones. Tone ReM-DoM (Figures 4 and 5).
- *Track 5.* In the first part of the theme, the triplets of bases are spliced into two tracks. In one of them, the first base of the triplet is represented (bass); in the second, the 2<sup>nd</sup> and 3<sup>rd</sup> base (percussion). Bar 3/4 and tone Mim (Figures 6 to 8).
- *Track 6.* The bases of the connexin DNA sequence (its alterations cause deafness) are represented by different bell sounds (Figures 1 to 3).
- *Track 7.* Guitar sounds are used as homage to the discovery of this gene by Nombela's group. The bases that can be heard are celtic drum, breathing, box and other effects save for the *obstinato* that results from a sequence fragment of repeated glutamines, for which we use a bass for one of the genomic bases to enhance this section. Tone DoM with a section in MibM and back to DoM (Figures 9 to 11).

- *Track 8.* The elements corresponding to the genetic material are low and consistent with the piano chords intertwined with harp designing the same harmony, by assigning to the first letter of the triplet the bass sound and to the two following ones the chord corresponding to the diatonic scale of DoM. Piano orchestration, harp accompanying flute, celtic flute and string. Tone DoM.
- *Track 9.* The bases of the genomic sequence are represented by a high percussion 1 and 2 and drum 1 and 2. String, vocals, lire, horns orchestration. Tone DoM.

- *Track 10.* In this theme we added to the basic genomic sequence of bases (in percussion), another sequence corresponding to amino acids, whose families are represented by different notes in celtic flute (Figure 12).

**Results**

Results are presented in figures 1 to 12.



Figure 1. Intuitive translation of bases ACGT or nucleotids of the Connexin sequence, the alteration of which causes deafness, to musical keys La, Do, Sol, Re.

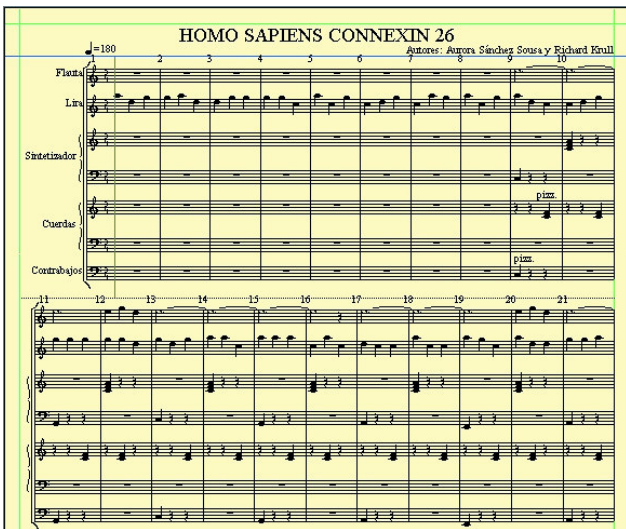


Figure 2. Connexin 26. On a base of bass and string is the genome with different bell sounds (2nd score); on it a flute melody. Tone DoM.

atg gat tgg ggc acg ctg cag acg atc ctg ggg ggt gtg aac aaa cac tcc acc  
 agc att gga aag atc tgg ctc acc gtc ctc ttc att ttt cgc att atg atc ctc gtt gtg  
 gct gca aag gag gtg tgg gga gat gag cag gcc gac ttt gtc tgc aac acc ctg cag  
 cca ggc tgc aag aac atg tgc tac gat cac tac ttc ccc atc tcc cac atc cgg cta  
 tgg gcc ctg cag ctg atc ttc gtg tcc agc cca ggc ctc cta gtg gcc atg cac gtg  
 gcc tac cgg aga cat gag aag aag agg aag ttc atc aag ggg gag ata aag agt  
 gaa ttt aag gac atc gag gag atc aaa acc cag aag gtc cgc atc gaa ggc tcc  
 ctg tgg tgg acc tac aca agc agc atc ttc ttc cgg gtc atc ttc gaa gcc gcc ttc atg  
 tac gtc ttc tat gtc atg tac gac ggc ttc tcc atg cag cgg ctg gtg aag tgc aac gcc  
 tgg cct tgt ccc aac act gtg gac tgc ttt ttg tcc cgg ccc acg gag aag act gtc ttc  
 aca gtg ttc atg att gca gtg tct gga att tgc atc ctg ctg aat gtc act gaa ttg ttg  
 tat ttg cta att aga lat tgt tct ggg aag tca aaa aag cca gtt taa

Figure 3. DNA sequence of Connexin 26.

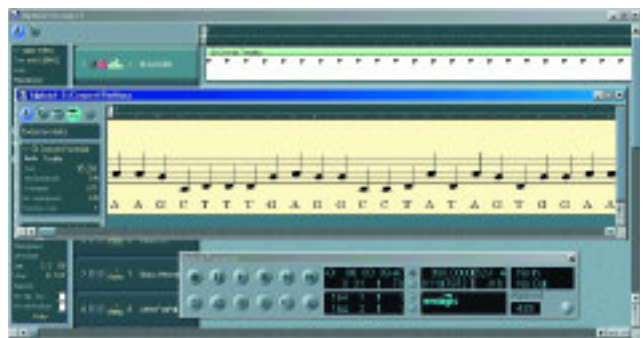


Figure 4. DNA sequence of Chromosome 20 (Alphoid sequence). It does not codify protein. Tone ReM- DoM.

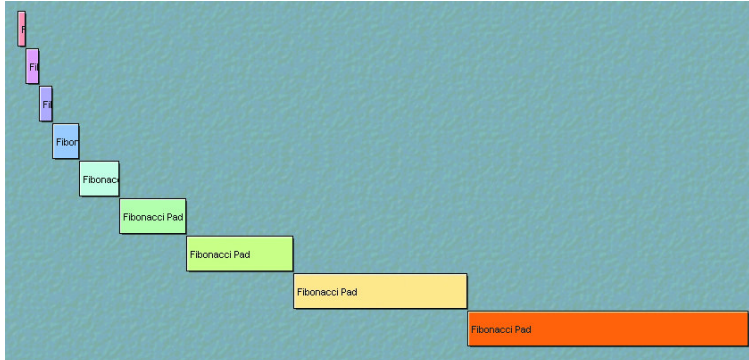


Figure 5. Low pitched blast (blowing sounds) note lengths assignation in a distinct key in accordance with Fibonacci's series (golden number). It starts with very low genome sounds followed by a rising pitch.

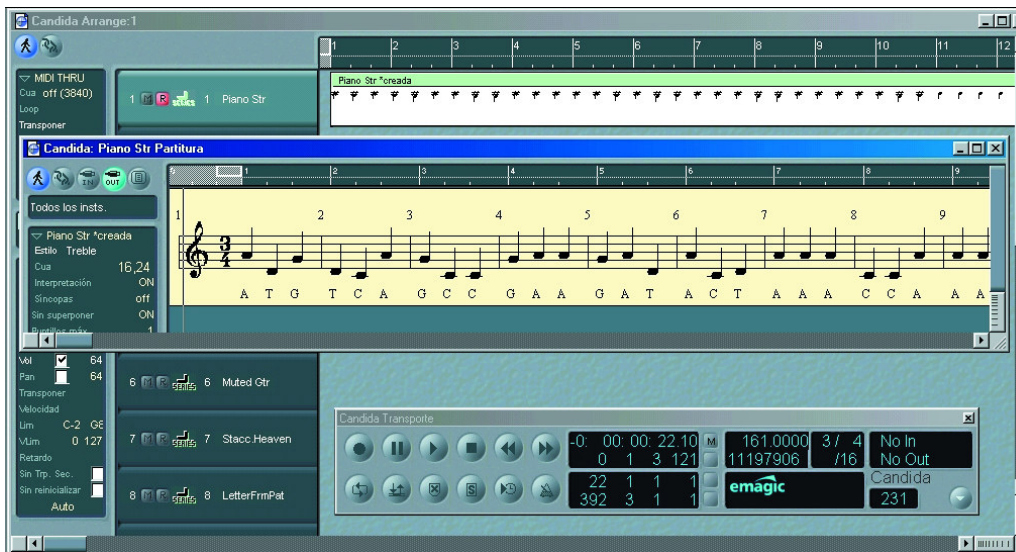


Figure 6. YRB1 (*C. albicans*). Intuitive translation. A = la, C = Do, G = sol, T = re

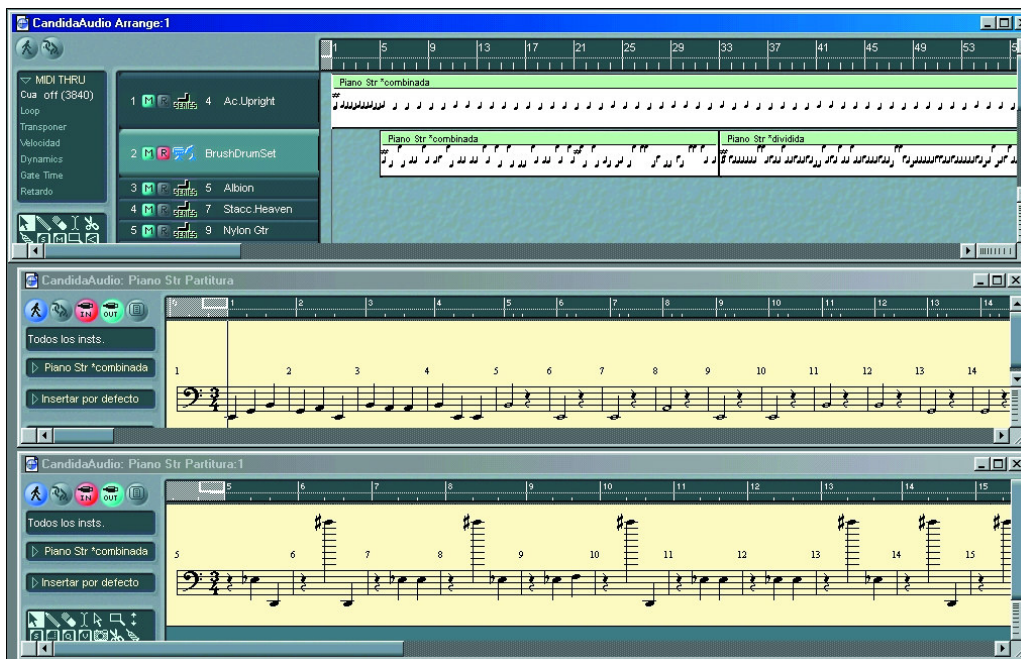


Figure 7. YRB1 (*C. albicans*). The genome supports the melody. The guitar rests on the genomic melody. Tone, Mim. 266 A = mi, 182 T = sol, 120 G = si, 83 C = la.



Discussion

The peculiarities of working with genes or coding sequences in the majority of the tracks has somewhat forced us to translate the nucleotide bases, to use ternary compasses so that the exact representation of the gene is maintained. This has entailed a rigorous work discipline, only allowing us more freedom with regard to other divisions of the musical tempo (binary tempo o 4 by 4 compass) in those cases that the sequences did not code for a protein.

The translation of amino acids is represented by musical notes (do, re, mi, fa, sol, la) of the different amino acid families (glutamate, aspartate, aromatic, serine, piruvate and histidine), vis-a-vis a translation of the 4 nucleotides (adenine, cytosine, guanine, thymine) coupled in groups of three as in the case of BCO. The simultaneous translation of nucleotides and amino acids has again made us use ternary compasses. If in the future we were to work only with amino acids, we would enjoy more work freedom. We would also translate the protein as an end product, and the concept would be different from the initial work layout.

By applying the golden number or Fibonacci sequence to a non-coding genomic sequence such as the alpoide we could obtain a very attractive aesthetic theme with lengthy notes in different tones. This musical technique was used by Bartok to develop a scale and also either intentionally or intuitively by Beethoven in his celebrated Fifth Symphony.

The application of mathematical methods to musical composition sometimes shows how an intimate relationship between both approaches can be achieved. This is the case of the "musical game of dices" by Mozart, when he composed a 16 compass waltz based on the addition of the aleatorious results obtained with two dices. Our musical work also attempts to reconcile science and music, with a relevant role for the inspiration of the composer.

Recent work such as Joan Guinjoan's piano composition, Verbum (October 2003), has been inspired by a gene related to human speech that evokes the DNA double helix on the basis of the progression of harmonic and melodic marches as well as the fragments integrated by 20 sounds or chords inspired by the description of amino acids [33].

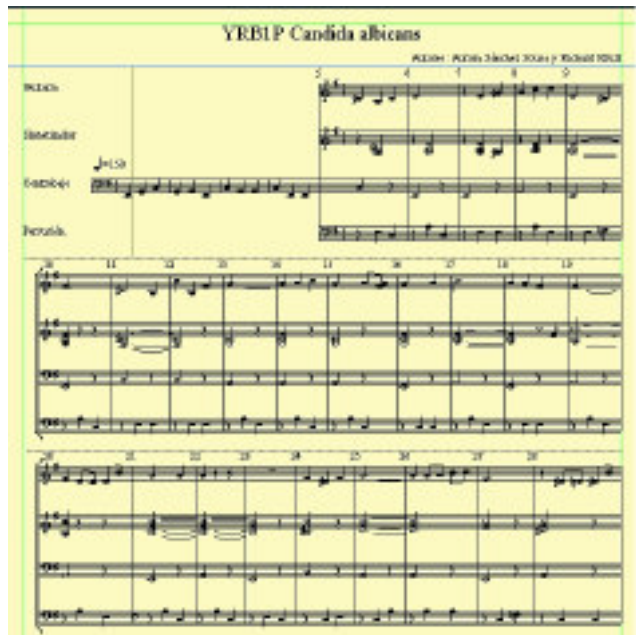


Figure 8. YRB1 (*C. albicans*). In the first four compasses we only hear the gene with a bass sound, and subsequently we hear the first triplet base with a bass sound and two different percussions in a different band from the other two bases. Rythm 3/4.

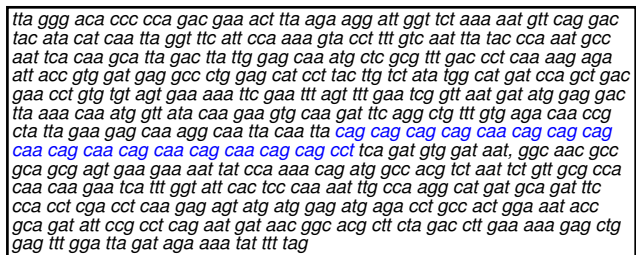


Figure 9. DNA sequence of SLT2 (*S. cerevisiae*) gene. Repetition of the triplet cag, caa (in blue), a true obstinato of the repeated amino acid, glutamine. Sounds for the bases, percussion and effects.

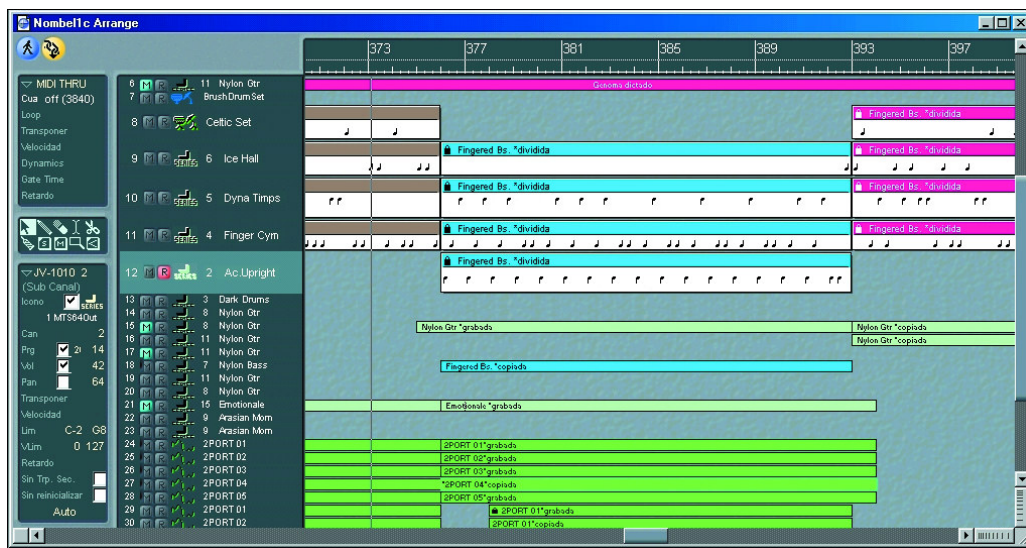


Figure 10. SLT2 (*S. cerevisiae*). Image of the obstinato where we have replaced the percussion sound of cytosine with a bass sound, to highlight the 17 compasses 376-392.

The composer Thilo Krigar has also been working on “DNA in Concert”. He uses the atoms that compose the DNA molecule as a starting point to convert the number of outer valence or total electron of hydrogen, carbon, nitrogen, oxygen and phosphorus into an equivalent number of semitone steps [24,25].

The Genoma Music Project has entered into other fields or different matters (Genoma Music 2, Genoma Music 3), working with other parameters and setting other challenges which were performed during Madrid’s “Week of Science” (November 2003 and 2004).

## Conclusion

A genome is not a mere aggregation of hundreds, thousands or a higher number of genes. There is a harmonic design, a grouping of genetic structures that determines an interdependent and well coordinated function, both structure and function concur in time and space, the regulation of these components is directed towards the participation of all genes and regulatory elements in a “cellular concert”. There is a rational basis – understanding DNA is to look deeper into rational Biology - and simultaneously there is a result that is creative, that is totally unexpected, in the function of organisms and cells in the environment where they operate. The genomic and proteomic technology will continue to bring us to the understanding of these phenomena.

We can also speak from the structure of the genes in a universal language that is represented by music. It is necessary to use working patterns that are rational, ordered and technically well developed in order to contribute something to the music of genome. But, on this basis there is room for the imagination, the feeling and the creativeness of the composer.

The Genoma Music project is endeavouring to bring music nearer to science, transmit sensations and feelings and to reach a harmony that is so necessary in the milieu of our lives.

Figure 11. Music score of *SLT2* with 1455 genomic notes grouped in 485 ternary compasses (rhythm 3/8).

Figure 12. In this track, “Omega basic component”, we obtain a score by representing a fictitious gene, where the nucleotide triplets correspond to a diversity of aminoacids. In the lower pentagram, the nucleotidic bases are described in a basic rhythm using percussion sounds. In the upper pentagram, a new note is found that corresponds to the type of aminoacid encoded by the triplet below. The sound of the amino acid series is described by celtic flute, and each of its notes clearly corresponds to a triplet of nucleotides in the lower pentagram. Composers: A. Sánchez Sousa, R. Krull, and F. Baquero.

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